

! Sequence: momp
 ! Sequence: incC
 ! Sequence: pomp91a
 CLUSTAL W (1.83) multiple sequence alignment

momp	-----
incC	-----
pomp91a	MKQMRLWGFELFLSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTKTTYSLRKDF
momp	-----
incC	-----
pomp91a	IVCDFAGNSIHKGAAFLNLKGDLFFINSTPLAALTFKNIHLGARGAGLFSESVNTFKGL
momp	-----
incC	-----
pomp91a	NPAEPSLMIDGILWEGFGGDPCDPCATWCDAIISMRVGGYGDVF SSGDASFLAEQPQLPSTSESQLVTQLLTMKHTQALSETVLQQ HSLVLENNESWGGVLTTSGDLSFINNTSVLCQNNISYGGGALLLQGRKSKALFFRDNRG
momp	-----
incC	-----
pomp91a	DRVLIKTDVNKEFQMGAKPTTDGNSAAPS QRDRLIPTASIIQLQVGGAAFTGGAGAPFQPG TILFLKNKAVNQDESHPGYGGAVSISPGSPITFADNQEILFQENEGELGGAIYNDQGAI
momp	-----
incC	-----
pomp91a	TLTARENPAYGRHMQDAEMFTNAACMALNIWDR PADDHRRHPIPPPVVPAQIETEITTIRSELQLMR TFENNQTTSSFSNKASFEELSIAATAISIHSGAIPYSLKTLQKLGGAIYHADYVHIRDC
momp	-----
incC	-----
pomp91a	FDVFCTLGATSGYLKGNSASFNLVGLFGDNENQRTVKAESVPNMSFDQSVVELYDTT STLQQSTKGARTGVVVTAJLMTISLLAIYIILAVLGFTEVLPQVALIMQGETN KGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHAN
momp	-----
incC	-----
pomp91a	FAWSVGARAALWECGCATLG LIWAMVGSIIICFLIALIG QGDIEFCGNKVRSQFHSHINSTSNFTNNAITIQGAPREF\$LSANEGRICFYDPIISATE
momp	-----
incC	-----
pomp91a	NYNSLYINHQLLEAGGAVIFSGARLSPEHKKENKNTSIINQPVRLCSGVLSIEGGAIL
momp	-----
incC	-----
pomp91a	ASFQYAQSKEPKVEELNVLCNAAEF TLGLLITNKNNTPLPAS AVRSFYQEGGLLAIGPGSKLTQGKNSEKDKitVITNLGFNLENLDSSDPAEIRATEKASI
momp	-----
incC	-----
pomp91a	TINKPKGYVGKEFFPLDLTAGTDAATG EISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVAPSPEKDIONLIIAESEYMG
momp	-----
incC	-----
pomp91a	TKDASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFADTIRIA YGYQGSWEFSWSPNDTKEKTTIISWTPPTGEFSLDPKRRGSFIPPTLWSTFSGLNIAASNI
momp	-----
incC	-----
	QPKSATAIFDTTILNPTIAGAGDVKTGAEGCQLGDTMQIVSLQLNKMRSRKSCGIAVGTTI

pomp91a	VNNNYLNNSEVIPLQHLCVFGGPVYQIMEQNPQSSNNLLVQHAGHNVGARI PFSFNTIL
momp incC pomp91a	VDADKYAVTVETRLIDERAAHVNAQFRF----- ----- SAALTQLFSSSSQQNVADKSHAQILIGTVSLNK\$WQALS1RSSF SYTEDSQVMKHVF PYK
momp incC pomp91a	----- ----- GTSRGSWRNYGWSGSVGM SYA YPKGIRYI LKMTPFV DILQYTKLVQNP FVETGYDPRYFSSS
momp incC pomp91a	----- ----- EMTNLSLPIGIALEMRFIGSRSSLFLQVSTS YIKDLRRVNPQSSASLVLNHYTW DIQGVP
momp incC pomp91a	----- ----- LGKEALNITLNSTIKYKIVTAYM GISSTQREGSNLSANA HAGLSLSF

“*” means that the residues or nucleotides in that column are identical in all sequences in the alignment

“:” means that conserved substitutions have been observed

“.” means that semi-conserved substitutions are observed

6693087pomp91a seq
LOCUS AAS37561 947 aa linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6693087.
ACCESSION AAS37561
VERSION AAS37561.1 GI:42715796
DBSOURCE accession AAS37561.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (residues 1 to 947)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding POMP91A protein of Chlamydia
JOURNAL Patent: US 6693087-A 3 17-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6693087
FEATURES Location/Qualifiers
source 1..947
/organism="unknown"
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121 hslvlenes wggvlttsgd lsfnnntsvl cqnnisyppg galllqgrks kalfrrdnrg
181 tillfknkav ndeshpgyg gavssispgs pitfadnqe1 lfgenege1 gaiyndggai
241 tfennnfqts ffsnkasfee lsaataaisi hsgaipyslk tllqk1ggai hadyvhirdc
301 kgsivfeens ataggaiavn avcdinaqgp vrfiinnsalg lnggaiymqa tgsi1rlhan
361 qgdiefcgnk vrsqfhshin stsnftnnai tiqqaprefs lsaneghric fydp1isate
421 nynslyinhq r11eaggavi fsgarlspeh kkenknktsi inqpvrlcsg v1siegmail
481 ayrsfyqegg l1algpqskl ttqgknsek1 kivitnlgfn lenldssdpa eiratekasi
541 eisgvprvyg htestyenhe yaskpyttsi ilsakk1vta psrpekd1qn l1iaeseymg
601 ygyqgswefs wspndtkekk t1iaswtp1g efs1dpkrrq sf1pttlwst fsq1niasni
661 vnnny1nse viplqh1cvf ggpvyq1meq npkqssnn11 vqhagh1rvga ripfsfntil
721 saaltqlfss ssqqnvadks haq1l1gtvs l1nkswqals1 rssfsyteds qvmkhvfp1k
781 gtsrgswrny gwsgsvgmsy aypkg1rylk mtpfvdlqyt k1vqnpfvet gydp1ryfsss
841 emtn1slpig ja1emrtf1gs rss1flqvst syikd1rrvn pqssas1v1n hytwdiqgvp
901 lgkealn1t1 nstiky1k1t1 aymg1s1t1qr egsn1sanah ag1s1sf

6686339incc seq
LOCUS AAS33023 203 aa Linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6686339.
ACCESSION AAS33023
VERSION AAS33023.1 GI:42707452
DBSOURCE accession AAS33023.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (Residues 1 to 203)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding inclusion membrane protein C of
Chlamydia
JOURNAL Patent: US 6686339-A 3 03-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6686339
FEATURES Location/Qualifiers
source 1..203
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61 siilqvggap tggagapfqp gpaddhhhpri pppvvpaqie teittirsel qlmrstlqgs
121 tkgartgvlv vtaiimtisi laiiiiilav lgftgvlpqv allmqgetnl iwamvsgsii
181 cfialigtg liltnkntpl pas

LOCUS Q46409 Stephens momp
 DEFINITION 393 aa Linear BCT 02-MAY-2006
 ACCESSION Major outer membrane protein, serovar D precursor (MOMP).
 VERSION Q46409
 DBSOURCE swissprot: locus OM1D_CHLTR, accession Q46409;
 class: standard.
 created: May 30, 2000.
 sequence updated: Nov 1, 1996.
 annotation updated: May 2, 2006.
 xrefs: X62918.1, CAA44701.1, AF063195.2, AAC31436.2, AE001273.1,
 AAC68276.1, H71484
 xrefs (non-sequence databases): PHCI-2DPAGE:Q46409,
 GenomeReviews:AE001273_GR, InterPro:IPR000604, Pfam:PF01308,
 PRINTS:PR01334
 KEYWORDS Complete proteome; Ion transport; Membrane; Outer membrane; Porin;
 Signal; Transmembrane; Transport.
 SOURCE Chlamydia trachomatis
 ORGANISM Chlamydia trachomatis
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCE 1 (residues 1 to 393)
 AUTHORS Sayada,C., Denamur,E. and Elion,J.
 TITLE Complete sequence of the major outer membrane protein-encoding gene
 of Chlamydia trachomatis serovar Da
 JOURNAL Gene 120 (1), 129-130 (1992)
 PUBMED 1398119
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=D/B-120
 2 (residues 1 to 393)
 AUTHORS Stothard,D.R., Boguslawski,G. and Jones,R.B.
 TITLE Phylogenetic analysis of the Chlamydia trachomatis major outer
 membrane protein and examination of potential pathogenic
 determinants
 JOURNAL Infect. Immun. 66 (8), 3618-3625 (1998)
 PUBMED 9673241
 REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 STRAIN=D/IU-71960
 3 (residues 1 to 393)
 AUTHORS Stephens,R.S., Kalman,S., Lammel,C., Fan,J., Marathe,R.,
 Aravind,L., Mitchell,W., Olinger,L., Tatusov,R.L., Zhao,Q.,
 Koonin,E.V. and Davis,R.W.
 TITLE Genome sequence of an obligate intracellular pathogen of humans:
 Chlamydia trachomatis
 JOURNAL Science 282 (5389), 754-759 (1998)
 PUBMED 9784136
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STRAIN=D/UW-3/CX
 COMMENT On Sep 27, 2005 this sequence version replaced gi:7442973.
 [FUNCTION] Structural rigidity of the outer membrane of elementary
 bodies and porin forming, permitting diffusion of solutes through
 the intracellular reticulate body membrane.
 [SUBUNIT] Disulfide bond interactions within and between MOMP
 molecules and other components form high molecular-weight
 oligomers.
 [SUBCELLULAR LOCATION] Bacterial cell outer membrane; multi-pass
 membrane protein.
 [SIMILARITY] Belongs to the chlamydial OMP family.
 FEATURES Location/Qualifiers
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 /db_xref="taxon:813"
 gene 1..393
 /gene="ompA"
 /locus_tag="CT_681"

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Protein
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  /locus_tag="CT_681"
  /product="Major outer membrane protein, serovar D
precursor"
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  /locus_tag="CT_681"
  /region_name="Signal"
  /inference="non-experimental evidence, no additional
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  /note="By similarity."
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  /locus_tag="CT_681"
  /region_name="Mature chain"
  /experiment="experimental evidence, no additional details
recorded"
  /note="Major outer membrane protein, serovar D.
/FTId=PRO_0000020147."
ORIGIN
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  61 rvgyygdvf v drvlktdvnk efqmgakptt dtgnsaapst ltarenpayg rhmqdaemt
  121 naacmalniw drfdvfctlg atsgylkgns asfnlvlgf dnengktvka esvpnmsfdq
  181 svvlelytdtt fawsgvraaa lwecgcattlg asfqyaqskp kveelnvln aaeftinkpk
  241 gyvgkefpld ltagtdaattg tkdasidyhe wqasla lsyr lnmftptyigv kwsrasfdad
  301 tiriqaqpksa taifdttln ptiagagdvk tgaegqlgdt mqivs lqlnk mksrkscgia
  361 vgtrivdadk yavtvetvli deraahvnaq frf

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